CC CKR2B   MLSTSRSRFIRNTNESGEEV--TTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLLFLITIPLWAH-SAANEWVF

CC CKR5   MDYQV-SSPIYDINYYTSEPCQKINVKQIANRLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQ-WDF

CC CKR1   METENTTEDYDTT----EFDYGDATPCQKVNERAFGAQLLPPLYSLVFVIQLVGNILVVLVLVQYKRLKNMTSIYLLNLAISDLLFLFTLPFWIDYKLKDDWVF
                                                                                                            I   II

            GNAMCKLFTGLYHIGYFGGIPFIILLTIDRYLAIVHAVTALKARTVTFGVVTSVITWLVAVTASVPGIIFTKCQKEDSVYVCGPYFPRG----WKNFBTIMRNILGLVLPLLIMVICYSGILKTLLRCR
            GRTHCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVTALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCR
            GDAMCKILSGFYYTGLYSEITFFILLTIDRYLAIVHAVFALRARTVTFGVITSIIIWALILASMPGLYFSKTQWEFTHHTCSLHFPHESLREWKLFQALKLNLFGLVLPLLVMIICYTGIKLLRRP
                  III   IV   V

            NEKKRHRAVRVIFTINIVYFLFWTPYNIVLLLNTFQBFFGLSNCESTSQLDQATQVTETLGMTBCCINPIIYAFVGBKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL
            NEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLLNTFQBFFGLNNCSSSNRLDQAMQVTBTLGMTBCCINPIIYAFVGBKFRNYLLVZPQKLAKRFCKCCSIFQQEAPERASSVYTRSTGBQEISVGL
            NBKKS-KAVRLIFVIMIIFFLFWTPYNLTILISVTQDPLFTBHCEQSRHLDLAVQVTEVIAYTBCCVNPVIYAFVGERFRKYLRQLFHRRVAVHLVKWLPPLSVDRLERVSSTSP-STGBHELSAGF
                 VI   VII

FIGURE 1A

```
        1                                  31        11
GAT CCG TCG ACC GCC ATT ATG GAT GGA TGG CAA GAA ACT CTC CCT CCG TGG AAC AAG ATG
asp pro ser thr ala ile met asp gly trp gln glu thr leu pro gly trp asn lys met
 61  /  21                               91   -31
GAT TAT CAA GTC TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA TCG GAG CCC TGC CAA
asp tyr gln val ser ser pro ile tyr asp ile asn tyr tyr thr ser glu pro cys gln
121  /  41                              151  /  51
AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC
lys ile asn val lys gln ile ala ala arg leu leu pro pro leu tyr ser leu val phe
181  /  61                              211  /  71
ATC TTT GGT TTT GTG GGC AAC ATG CTC GTC ATC CTC ATC CTA AAC TGC AAA AGG CTC
ile phe gly phe val gly asn met leu val ile leu ile leu ile asn cys lys arg leu
241  /  81                              271  /  91
AAG AGC ATG ACT GAC ATC TAC CTC CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT CTT
lys ser met thr asp ile tyr leu leu asn leu ala ile ser asp leu phe phe leu leu
301  /  101                             331  /  111
ACT GTC CCC TTC TGG GCT CAC TAC TTG GCC GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT
thr val pro phe trp ala his tyr leu ala ala gln trp asp phe gly asn thr met cys
361  /  121                             391  /  131
CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC TTC TCT CGA ATC TTC TTC ATC ATC CTC
gln leu leu thr gly leu tyr phe ile gly phe phe ser gly ile phe phe ile ile leu
421  /  141                             451  /  151
CTG ACA ATC GAT AGG TAC CTG GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG
leu thr ile asp arg tyr leu ala val val his ala val phe ala leu lys ala arg thr
481  /  161                             511  /  171
GTC ACT TTT GGG GTG GTG ACA AGT CTC ATC ACT TGG GTG GTC GCT GTG TTT GCG TCT CTC
val thr phe gly val val thr ser val ile thr trp val val ala val phe ala ser leu
541  /  181                             571  /  191
CCA GGA ATC ATC TTT ACC ACA TCT CAA AAA GAA GGT CTT CAT TAC ACC TGC ACC TCT CAT
pro gly ile ile phe thr arg ser gln lys glu gly leu his tyr thr cys ser ser his
601  /  201                             631  /  211
TTT CCA TAC AGT CAG TAT CAA TTC TGG AAG AAT TTC CAG ACA TTA AAG ATA GTC ATC TTG
phe pro tyr ser gln tyr gln phe trp lys asn phe gln thr leu lys ile val ile leu
661  /  221                             691  /  231
GGG CTG GTC CTC CCG CTG CTT GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA ACT CTG
gly leu val leu pro leu leu val met val ile cys tyr ser gly ile leu lys thr leu
721  /  241                             751  /  251
CTT CGG TGT CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC ATG
leu arg cys arg asn glu lys lys arg his arg ala val arg leu ile phe thr ile met
781  /  261                             811  /  271
ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC AAC ATT GTC CTT CTC CTG AAC ACC TTC CAG
ile val tyr phe leu phe trp ala pro tyr asn ile val leu leu leu asn thr phe gln
841  /  281                             871  /  291
GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT AAC AGG TTG GAC CAA GCT ATC CAG GTG
glu phe phe gly leu asn asn cys ser ser ser asn arg leu asp gln ala met gln val
901  /  301                             931  /  311
ACA GAG ACT CTT GGC ATC ACG CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG
thr glu thr leu gly ile thr his cys cys ile asn pro ile ile tyr ala phe val gly
961  /  321                             991  /  331
GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC TGC
glu lys phe arg asn tyr leu leu val phe phe gln lys his ile ala lys arg phe cys
1021 /  341                             1051 /  351
AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC TCA GTT TAC ACC CGA
lys cys cys ser ile phe gln gln glu ala pro glu arg ala ser ser val tyr thr arg
1081 /  361                             1111 /  371
TCC ACT GGG GAG CAG GAA ATA TCT GTC GGC TTG TGA CAC CGA CTC AAG TGG GCT GGT GAC
ser thr gly glu gln glu ile ser val gly leu OPA his gly leu lys trp ala gly asp
1141 /  381                             1171 /  391
CCA CTC AGA GTT GTC CAC ATG GCT TAG TTT TCA TAC ACA GCC TGG GCT GGC GCT GGG GTG
pro val arg val val his met ala AMB phe ser tyr thr ala trp ala gly gly gly val
1201 /  401                             1231 /  411
GCA GAG CTC TTT TTT AAA AGG AAG TTA CTG TTA TAG ACG GTC TAA GAT TCA TCC A7
gly glu val phe phe lys arg lys leu leu leu AMB arg val OCH asp ser ser
```

FIGURE 1B

Figure 1C

SEQ ID NO:3

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   1 aagaaactct ccccgggtgg aacaagatgg attatcaagt gtcaagtcca atctatgaca
  61 tcaattatta tacatcggag ccctgccaaa aaatcaatgt gaagcaaatc gcagcccgcc
 121 tcctgcctcc gctctactca cgggtgttca tcttggttt tgtgggcaac atgctggtca
 181 tcctcatcct gataaactgc aaaaggctga agagcatgac tgacatctac ctgctcaacc
 241 tggccatctc tgacctgttt ttccttctta ctgtcccctt ctgggctcac tatgctgccg
 301 cccagtggga ctttggaaat acaatgtgtc aactcttgac agggctctat tttataggct
 361 tcttctctgg aatcttcttc atcatcctcc tgacaatcga taggtacctg gctgtcgtcc
 421 atgctgtgtt tgctttaaaa gccaggacgg tcacctttgg ggtggtgaca agtgtgatca
 481 cttgggtggt ggctgtgttt gcgtctctcc aggaatcat ctttaccaga tctcaaaaag
 541 aaggtcttca ttacacctgc agctctcatt ttccatacag tcagtatcaa ttctggaaga
 601 atttccagac attaaagata gtcatcttgg ggctggtcct gccgctgctt gtcatggtca
 661 tctgctactc gggaatccta aaaactctgc ttcggtgtcg aaatgagaag aagaggcaca
 721 gggctgtgag gcttatcttc accatcatga ttgtttattt tctcttctgg gctccctaca
 781 acattgtcct tctcctgaac accttccagg aattctttgg cctgaataat tgcagtagct
 841 ctaacaggtt ggaccaagct atgcaggtga cagagactct tgggatgacg cactgctgca
 901 tcaaccccat catctatgcc tttgtcgggg agaagttcag aaactacctc ttagtcttct
 961 tccaaaagca cattgccaaa cgcttctgca atgctgttc tattttccag caagaggctc
1021 ccgagcgagc aagctcagtt tacacccgat ccactgggga gcaggaaata tctgtgggct
1081 tgtgacacgg actcaagtgg gctggtgacc cagtcagagt tgtgcacatg gcttagtttt
1141 catacacagc ctgggctggg ggtggggtgg gagaggtctt ttttaaaagg aagttactgt
1201 tatagagggt ctaagattca tccat
```

SEQ ID NO:4

MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRL

KSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQ

LLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFAS

LPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGIL

KTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLD

QAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPER

ASSVYTRSTGEQEISVGL

FIGURE 2

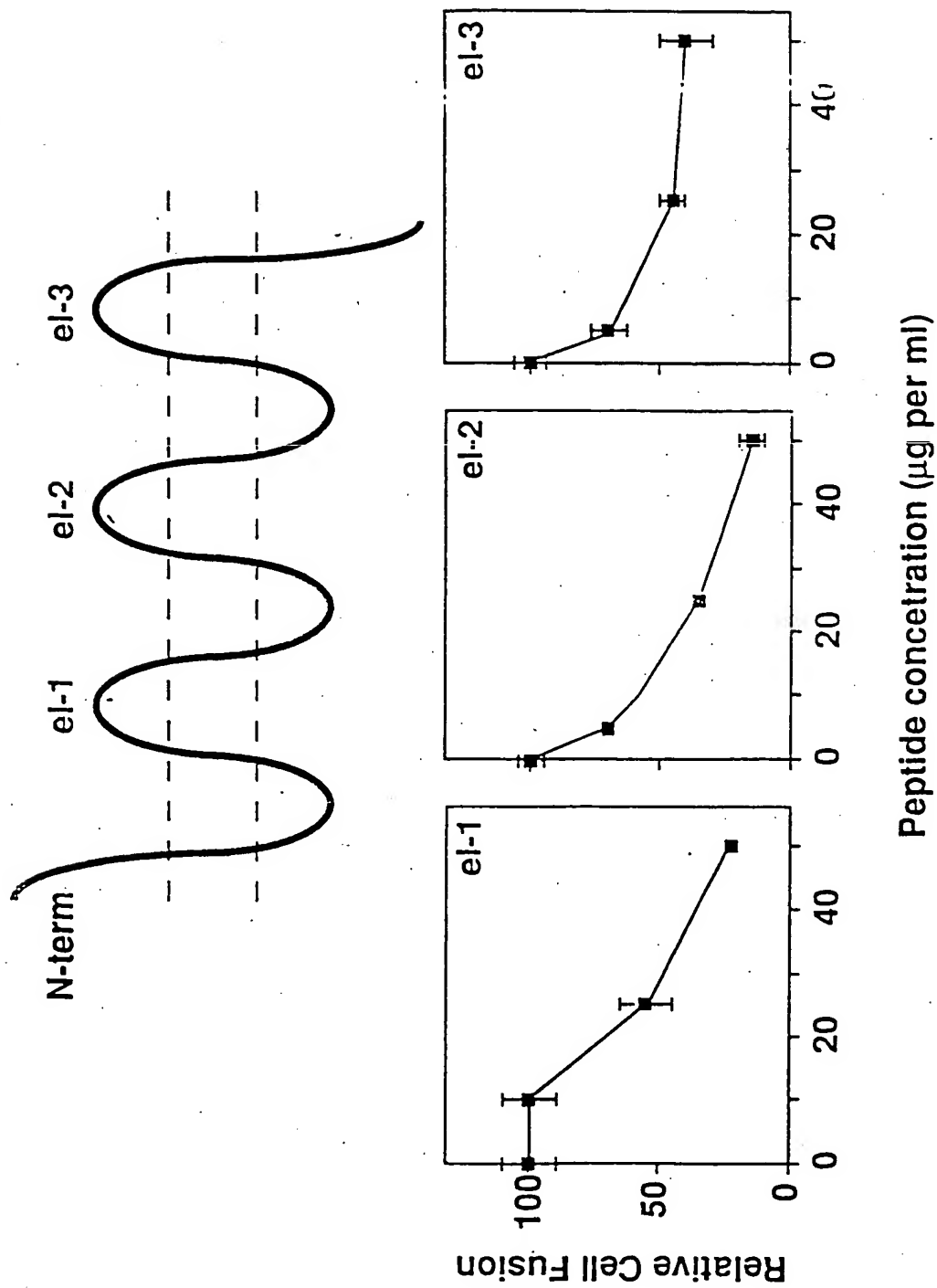Effects of CCR5 Synthetic Peptides on HIV Env-Mediated Fusion